

**THE EMBODIMENTS OF THE INVENTION IN WHICH AN EXCLUSIVE PROPERTY OF PRIVILEGE IS CLAIMED ARE DEFINED AS FOLLOWS:**

1. A nucleic acid molecule, or a derivative thereof, encoding a ROS repressor optimized for plant codon usage and exhibiting ROS operator binding activity, ROS repressor activity, or both ROS operator binding activity and ROS repressor activity.
2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule, or a derivative thereof, comprises greater than 80% similarity with the nucleotide sequence of SEQ ID NO:2 as determined by use of the BLAST algorithm with the following parameters: blastn; Database: nr; Expect 10; filter: low completness; Alignment: pairwise; Wordsize 11.
3. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule, or a derivative thereof, hybridizes under stringent conditions with the nucleotide sequence of SEQ ID NO:2, said stringent conditions comprising, hybridizing for 16-20 hrs at 65°C in 7% SDS, 1mM EDTA, 0.5M Na<sub>2</sub>HPO<sub>4</sub>, pH 7.2, followed by washing in 5% SDS, 1mM EDTA 40mM Na<sub>2</sub>HPO<sub>4</sub>, pH 7.2 for 30 min, followed by washing in 1% SDS, 1mM EDTA 40mM Na<sub>2</sub>HPO<sub>4</sub>, pH 7.2 for 30 min.
4. The nucleic acid molecule of claim 1 wherein said nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO:2.
5. A genetic construct comprising a regulatory region in operative association with the nucleic acid molecule of claim 1.
6. The nucleic acid molecule of claim 1, further comprising a nuclear localization signal fused to said nucleic acid molecule.
7. The genetic construct of claim 5, further comprising a nuclear localization signal fused to said nucleic acid molecule.

8. A plant comprising the genetic construct of claim 5.
9. A plant comprising the genetic construct of claim 7.
10. A seed comprising the genetic construct of claim 5.
11. A seed comprising the genetic construct of claim 7.
12. A nucleic acid molecule comprising a regulatory region operatively linked to a gene of interest and one, or more than one, ROS operator sequence capable of controlling the activity of said regulatory region, wherein said regulatory region is functional in plants.
13. The nucleic acid molecule of claim 12, wherein said at least one ROS operator sequence comprises the nucleotide sequence of SEQ ID NO:8.
14. A genetic construct comprising the nucleic acid molecule of claim 12.
15. A plant comprising the genetic construct of claim 14.
16. A plant comprising:
  - i) a first genetic construct comprising said genetic construct of claim 14, and
  - ii) a second genetic construct comprising a regulatory region in operative association with a nucleic acid molecule, or a derivative thereof, said nucleic acid or derivative thereof encoding a ROS repressor optimized for plant codon usage and exhibiting ROS operator binding activity, ROS repressor activity, or both ROS operator binding activity and ROS repressor activity.
17. The plant as defined in claim 16, wherein said second genetic construct further comprises a nuclear localization signal fused to said nucleic acid molecule or derivative thereof.

18. The nucleic acid molecule of claim 12, wherein said gene of interest encodes a protein selected from the group consisting of one or more enzymes involved in fiber biosynthesis, one or more enzymes involved in glucosinolate biosynthesis, one or more enzymes involved in phytotoxin biosynthesis, caffeic o-methyltransferase, indole acetamide hydrolase, and phosphinothricin acetyl transferase.

19. A method for selectively controlling the transcription of a gene of interest, comprising:

- i) producing a first plant comprising a first genetic construct, said first genetic construct comprising a first regulatory region operatively linked to a gene of interest and one, or more than one, ROS operator sequence capable of controlling the activity of said first regulatory region;
- ii) producing a second plant comprising a second genetic construct, said second genetic construct comprising a second regulatory region in operative association with a nucleic acid molecule, or a derivative thereof, encoding a ROS repressor, said ROS repressor exhibiting both ROS operator binding activity and ROS repressor activity;
- iii) crossing said first plant and said second plant to obtain progeny, said progeny comprising both said first genetic construct and said second genetic construct, and characterized in that the expression of said second genetic construct represses expression of said first genetic construct.

20. The method of claim 19, wherein said first and second regulatory regions are either the same or different and are selected from the group consisting of a constitutive promoter, an inducible promoter, a tissue specific promoter, and a developmental promoter.

21. A method for selectively controlling the transcription of a gene of interest in a plant, comprising:

- i) introducing into said plant:

- a) a first genetic construct comprising a nucleic acid molecule comprising a first regulatory region operatively linked to a gene of interest, and one, or more than one, ROS operator sequence capable of controlling the activity of said first regulatory region; and
- b) a second genetic construct comprising a second regulatory region in operative association with a nucleotide sequence encoding a ROS repressor, or a derivative thereof, said ROS repressor exhibiting both ROS operator binding activity and ROS repressor activity; said second regulatory region comprises an inducible promoter;

- ii) growing said plant, and
- iii) inducing the activity of said inducible promoter so that expression of said second genetic construct produces said ROS repressor and represses expression of said gene of interest.

22. A method for selectively controlling the transcription of a gene of interest in a plant, comprising:

- i) introducing into said plant:
  - a) a first genetic construct comprising a nucleic acid molecule comprising a first regulatory region operatively linked to a gene of interest, and one, or more than one, ROS operator sequence capable of controlling the activity of said first regulatory region; and
  - b) a second genetic construct comprising a second regulatory region in operative association with a nucleotide sequence encoding a ROS repressor, or a derivative thereof, said ROS repressor exhibiting both ROS operator binding activity and ROS repressor activity; said second regulatory region comprises a tissue specific promoter; and
- ii) growing said plant, so that expression of said second genetic construct produces said ROS repressor and represses expression of said gene of interest in a tissue specific manner.

23. A method for selectively controlling the transcription of a gene of interest in a plant, comprising:

- i) introducing into said plant:
  - a) a first genetic construct comprising a nucleic acid molecule comprising a first regulatory region operatively linked to a gene of interest, and one, or more than one, ROS operator sequence capable of controlling the activity of said first regulatory region; and
  - b) a second genetic construct comprising a second regulatory region in operative association with a nucleotide sequence encoding a ROS repressor, or a derivative thereof, said ROS repressor exhibiting both ROS operator binding activity and ROS repressor activity; said second regulatory region comprises a promoter that is active at one or more specific developmental stages within said plant; and
- ii) growing said plant, so that the activity of said promoter at one or more specific developmental stages within said plant results in expression of said second genetic construct thereby producing said ROS repressor, and represses expression of said gene of interest.

24. A method for selectively controlling the transcription of a gene of interest, comprising:

- i) producing a first plant comprising a first genetic construct, said first genetic construct comprising a first regulatory region operatively linked to a gene of interest and one, or more than one, repressor operator sequence capable of controlling the activity of said first regulatory region;
- ii) producing a second plant comprising a second genetic construct, said second genetic construct comprising a second regulatory region in operative association with a nucleic acid molecule, or a derivative thereof, encoding a repressor, said repressor exhibiting both repressor operator binding activity and repressor activity, and said repressor optimized for plant expression;
- iii) crossing said first plant and said second plant to obtain progeny, said progeny comprising both said first genetic construct and said second genetic construct,

and characterized in that expression of said second genetic construct represses expression of said gene of interest.

25. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule, or a derivative thereof, comprises greater than 80% similarity with the nucleotide sequence of SEQ ID NO:3 as determined by use of the BLAST algorithm with the following parameters: blastn; Database: nr; Expect 10; filter: low complexity; Alignment: pairwise; Wordsize 11.
26. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule, or a derivative thereof, hybridizes under stringent conditions with the nucleotide sequence of SEQ ID NO:3, said stringent conditions comprising, hybridizing for 16-20 hrs at 65°C in 7% SDS, 1mM EDTA, 0.5M Na<sub>2</sub>HPO<sub>4</sub>, pH 7.2, followed by washing in 5% SDS, 1mM EDTA 40mM Na<sub>2</sub>HPO<sub>4</sub>, pH 7.2 for 30 min, followed by washing in 1% SDS, 1mM EDTA 40mM Na<sub>2</sub>HPO<sub>4</sub>, pH 7.2 for 30 min.
27. The nucleic acid molecule of claim 1 wherein said nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO:3.
28. A vector comprising:
  - i) a first genetic construct comprising a first nucleic acid molecule comprising a first regulatory region operatively linked to a gene of interest and one, or more than one, ROS operator sequence capable of controlling the activity of said first regulatory region, wherein said first regulatory region is functional in plants; and
  - ii) a second genetic construct comprising a second regulatory region in operative association with a second nucleic acid molecule, or a derivative thereof, said second nucleic acid or derivative thereof encoding a ROS repressor optimized for plant codon usage and exhibiting ROS operator binding activity, ROS repressor activity, or both ROS operator binding activity and ROS repressor activity.

29. The vector as defined in claim 28, wherein said second genetic construct further comprises a nuclear localization signal fused to said second nucleic acid molecule or derivative thereof.
30. The vector of claim 28, wherein said first and second regulatory regions are either the same or different and are selected from the group consisting of a constitutive promoter, an inducible promoter, a tissue specific promoter, and a developmental promoter.
31. A plant comprising the vector of claim 29.
32. A plant comprising the vector of claim 30.
33. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule, or a derivative thereof, comprises greater than 80% similarity with the nucleotide sequence of SEQ ID NO:3 as determined by use of the BLAST algorithm with the following parameters: blastn; Database: nr; Expect 10; filter: low complexity; Alignment: pairwise; Wordsize 11.
34. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule, or a derivative thereof, hybridizes under stringent conditions with the nucleotide sequence of SEQ ID NO:3, said stringent conditions comprising, hybridizing for 16-20 hrs at 65 °C in 7% SDS, 1mM EDTA, 0.5M Na<sub>2</sub>HPO<sub>4</sub>, pH 7.2, followed by washing in 5% SDS, 1mM EDTA 40mM Na<sub>2</sub>HPO<sub>4</sub>, pH 7.2 for 30 min, followed by washing in 1% SDS, 1mM EDTA 40mM Na<sub>2</sub>HPO<sub>4</sub>, pH 7.2 for 30 min.
35. The nucleic acid molecule of claim 1 wherein said nucleic acid molecule comprises the nucleotide sequence of SEQ ID NO:3.
36. The nucleic acid molecule of claim 12, wherein said at least one ROS operator sequence comprises the nucleotide sequence of SEQ ID NO:20.